

FIGURE 1

Fucosyltransferase nucleotide sequence from strain 1182 FutB (SEQ ID NO:1)

Protein sequence from strain 1182 FutB (SEQ ID NO:2)

mfqplldayiesasiekitsksppplkiavanwwgdeeveefkknilyfilsqhyytitlhqnepSDLVfgspigsarkilsy
qnakrvfytgenespnfnlfdfaigfdeldfrdrylmplyydrllhhkaesvndtspyklkpdslyalkkpshhfkenhpnl
cavvnnesdplkrgfasfvasnnpaprknafydvlnsiepviggsvkntlgyniknkseflsqykfnlcfcensqgygyte
kiidayfshtipiwygspsvaqdfnpksfvnvcdfkdfdeaidhvrylhthpnayldmlyenplntldgkayfyqnlsfkki
ldffktilendtiyhdnpfifyrdlneplisiddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlrvnydd
lrvnyddlrvnyddlrvnyddlrvnyyerllqnasppllelsqntfkiyrkayqkslplraarklikklgl*

FIGURE 2

Fucosyltransferase from strain 1111 FutA

Nucleotide coding sequence (SEQ ID NO:3)

atgttccaacccctattagatgccttatagaagcgctccattgaaaaaatggcctaaatctccccccctaaaatcgctgtgg
cgaattggggagatgaagaaattaaaaatttaaaaagagcgttcttatttatcctaagccaggattacacaatactttaca
ccgaaacctgataaacctgcggacatcgctttgttaacccttgatcagccagaaaaatcttacccatcaaagcggaaaa
gggtgtttacccggtaaaatgaagtccctaactcaacccctttagtacgccataggcgtttagaattggacttttagagatcgt
tatttgagaatgccttgcattatgcctatttgcattaaagccgagcttgttaatgacaccacttcgccttataactccaaacctgaca
gccttacccatcattttaagaaaaaccaccccaatttgtgcgcagtagtgaataatgagagtgatcccttgc
aaaagagggttgcgagttgtcgaagcaaccctaacgcctttagaagggAACGCTTTATGAGGCTTAAACGCTATTGAGCC
AGTTGCTGGGGAGGGAGCCTGAAAAACACTTGTAGCTATAATGTCAAAACAAGAGCGAGTTTAAGCCAATAACAAATTCAAT
CTGTGTTGAAAACACTCAAGGCATGGCTATGTAACTGAAAAGATCATTGACGCTTACCCATACCATTCTATTGAGGG
AGTCCCAGCGTGGCGAAAGATTIAACCCCTAAAGAGTTGTGAATGCCATGATTCAACACTTGTAGAAGCGATGACTATATCA
GATACTGCACACGCACCCAAACGCTTACCCATGACATGCACATGAAAACCCCTTAAACACTATTGATGGGAAAGCTTACTTTACCA
AAATTGAGTTAAAAAAATCCTAGATTGTTAAACGATTGAGGAAACGACACGATCTACGATAACCCCTTCATTCTATCGTG
ATTGAAFGAGCCTCAGTATCTATTGATGGTTGAGGGTAATTGATGATTGAGGGTAATTGATGATTGAGGGTAATTGAT
GATTGAGGGTAATTGAGCGCCTTACAAACGCCCTGCCTTATTAGAACTCTCTCAAACACCACCTTAAATCTATCGCAAA
GCTTACCCATCCTGCCTTGTGCGTGCCTAAAGGAGATGGGTTAAAGTAA

Protein sequence (SEQ ID NO:4)

mfqplldafiesaplkkwplnlpplkiavanwwgdeeikkfkksvlyfilsqhyltitlhrnpdkpadivfgnplgsarkilsy
qnakrvfytgenepnfnlfdfaigfdeldfrdrylmplyayylhykaelvndtspyklqpdslyalkkpshhskenhpn
lcavvnnesdplkrgfasfvasnpnaprrnafyalealnaiepvaggsvkntlgynvknkseflsqykfnlcfentqgygyvt
ekiidayfshtipiywgspsvakdfnpksfvnhdfnnfdeaidyirylhthpnayldmhyenplntidgkayfyqnlfsk
kildffktilendtiyhdpnfifyrdlnepsvsidglrvnyddlrnvnyddlrnvnyerllqnaspllelsqnttfkiyrka
yqkslpllrairrwvkk*

FIGURE 3

Strain 1218 *FutB* nucleotide sequence (SEQ ID NO:5)

Predicted protein strain 1218 FutB (SEQ ID NO:6)

FIGURE 4

Fucosyltransferase strain 19C2 FutB nucleotide sequence (SEQ ID NO:7)

atgttccaacccatttagacgcttatagacagcaccgttagatgaaaccgattataagccccattaaatagccctagcg
aattgggtgccttgataaaagagaaagcaagggttagaaaaaaaattatcttacatttcatttaagtcagcattacacaatcgc
tctccaccgaaacctgataaacctgcggacatcggttttgtaaaccccttggatcagccagaaaaatcctatcctatcaaacg
ctaaaagggtgtttcacccggtaaaaacgaagtccctaattcaaccttgcattacgccataggcttgcattttgactttaga
gatcgttatttgcataatgatagactacaccataaagccgagagcgtgaatgacaccaccgcacccataagatt
aaatctgacagcccttatgccttaaaaaagccctccatcatttaaagaaaaccacccacattatgcgcgctaatcaataatgaga
tcgatcccttgcataaaaaagaggggttgcgagcttgcgaagcaaccctaacgccttataaggAACGCTTCTATGAGGCTTAAATT
tattgagccagttactggggagggagcgtgagaaacactttaggtataacgtcaaaaacaaaacgaattttgcacccat
aattcaatctgtgccttgcataaaaaacactcaaggctatggctatgttactgaaaaatcattgacgcctacttcagccacaccatcctat
ttattggggggagtcctagcgtggcgaaagatttaacccc

Strain 19C2 FutB protein sequence (SEQ ID NO:8)

mfqpIldayidstrldetdykpplnialanwwpldkreskgfrkkfilhfilsqhytialhrnpdkpadivfgnplgsarkilsy
qnakrvfytgenepnfnlfdfaigfdeldfrdrylrmplyydrlhkaesvndtapykiksdslyalkkpshhfkhenhph
lcalinneidplkrgfasfvasnnapirnafyealnsiepvtggsvrntlgynvknkneflsqykfnlcfcntqgygyvtek
iidayfshtipiywggvpsvakdfnp

FIGURE 5

Strain 915 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:9)

atggcctaaatctccccccctaaaaatcgctgtggcgaattggtggggagatgaagaaaattttaaaaagagcgttctttatttatctaagccaggcattacacaatcacttacaccgaaacctgataaacctgcggacatcgtcttgtaaccccttggatcagccagaaaaatcttatcctatcaaaacgcaaaaagggtgtttacaccggtaaaaatgaagtccctaactcaacctcttgattacgccataggctt

Protein sequence from Strain 915 FutA (SEQ ID NO:10)

maskspplkiavanwwgdeeikkfkksvlyfilsqhytitlhrnpdkpadivfgnplgsarkilsyqnakrvfytnenevpnfnlfdfaigf

FIGURE 6

Strain 26695 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:11)

Protein coding sequence Strain 26695 FutA (SEQ ID NO:12)

mfqplldafiesasiekmaskssppplkiavanhwgdeeiikefkksvlyfilsqryaitlhqnepnfsdlvfnplgaarkil
syqntkrvfytgenespnfnlfdfaigfdelfndrylrmplyyahlhykaelvndtapylkldnslyalkkpshhkenh
pnlcavvndesdlkrgfasfasnanapmrnafydalnsieptvggsvrntlgkvgnkseflsqykfnlcensqgygy
vtekildayfshtipiwygspsvakdfnpksfvnhdfnfddeaidyikylhthpnayldmlyenplntldgkayfyqdlsf
kkildffktilendtiyhkfstsfnweydlhkplvsiddrvnyddlrnvydrllqnaspllelsqnttfkiyrkayqksplrrav
rklvkkgl*

FIGURE 7

19C2A fucosyltransferase nucleotide sequence (SEQ ID NO:13)

atgttccaacccttactagacgccttatagaaagtgctccaatt

19C2A predicted protein sequence (SEQ ID NO:14)

mfqpplldafiesapi

FIGURE 8

Protein sequence from strain 1182 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	23	PPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI	81
Sbjct:	11	TVPLLLAIYTWWSLIEYKEWKSPIYFIGSQAPQPPLR---ILLWTWPNGNPLALSDCP	67
Query:	82	LSYQNAKRVFYTGEN---ESPNFNLF---DYAIGFDELDFRDRYLRLMPYYDRLHHKAES	135
Sbjct:	68	LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPGQPWVWASMESPNS	127
Query:	136	-VNDTTSPYKLKPDSLALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPN-AP	193
Sbjct:	128	GLNDLRDGYNWTLSYRADSDAFHPYGYLEPRLSQVVAAPLLSAKRKGAAWVVSNCNTRS	187
Query:	194	KRNAFYDVLSNIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGYVTEKIID	253
Sbjct:	188	KRERFYKQLNKHLQDVGGRVANPLPLKVGCIVETLSQYKFYLAFENSQHYDYVTEKLWK	247
Query:	254	-AYFSHTIPIYWGPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYL	305
Sbjct:	248	NALQAGTIPIVVLGPRAVYEDFVPPKSFIHVDDFKSPKEIADLYLDTNPTAYS	301

FIGURE 9

Fucosyltransferase from strain 1111 FutA aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	27	IAVANWWGDEEIKKFKKSVLYFILSQHYTITLHRNPDKPADIYFG-NPLGSARKILSYQN	85
Sbjct:	16	LAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWFNGNPLALSDCPLSYQN	72
Query:	86	AKRVFYTGEN---EVPNFNLF---DYAIGFDELDFRDRYLRLMPLYYAYLHYKAEL-VNDT	138
Sbjct:	73	TARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPPGQPWVWASMESPSNSGLNDL	132
Query:	139	TSPYKLQPDSDLYALKKPSSHFKENHPNLCAVVNNESDPLKRGFASFVASNPNA-APRRNAF	197
Sbjct:	133	RDGYFNWTLTSYRADSDAFHPYGYLEPRLSQVVAAPLLSAKRKGAAWVVSNCNTRSKRERF	192
Query:	198	YEALNAIEPVAGGGSVKNTLGYNVNKSEFLSQYKFNLCFENTQGYGYVTEKIID-AYFS	256
Sbjct:	193	YKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWKNALQA	252
Query:	257	HTIPIYWGPSVAKDFNPKS-FVNVHDFNNFDEAIDYIRYLHTHPNAYLDMHYENPLNTI	315
Sbjct:	253	GTIPVVLGPRAVYEDFVPPKSFIHVDDFKSPKEIADYLLYLDTNPTAYS-----	301
Query:	316	DGKAYFYQNLASFKKILDFFKTILENDTIYHDNPFIFYRDLNEPSVSIDGLRVNYDDLKV	375
Sbjct:	302	-----EYFEWRYDLRVRLFSDALR-----	321
Query:	376	YDDLRLVNYDDLRLVNYERLLQNASPLLELSQNTTFKIKYRKAYQ	417
Sbjct:	322	-----YDEGFCRVCRVLLQNP-----RYKTYPNIAKWFQ	351

FIGURE 10

Protein sequence from strain 1218 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	23	PPPLKIAVANWWGDEEVEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI	81
Sbjct:	11	TVPLLAIYTWWSLIEYKEWKSPIYFIGSQAPQPPLR---ILLWTWPFGNPLALSDCP	67
Query:	82	LSYQNAKRVFYTGEN---ESPNFLF---DYAIGFDELDFRDRYLRMPLYYDRLHHKAES	135
Sbjct:	68	LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPGQPVWASMESPSNS	127
Query:	136	-VNDTTSPYKLKPDSLYALKPSSHFKENHPNLCAVVNNESDPLKRGFASFVASNPN-AP	193
Sbjct:	128	GLNDLRLGYFNWTLSYRADSDAFHPYGYLEPRLSQVNVNAPLLSAKRKGAAWVVSNCNTRS	187
Query:	194	KRNAFYDALNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGYVTEKIID	253
Sbjct:	188	KRERFYKQLNKHQLQDVGGRVANPLPLKVGCIVETLSQYKFYLAFENSQHYDYVTEKLWK	247
Query:	254	-AYFSHTIPIYWGSPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYLDMLYEN	311
Sbjct:	248	NALQAGTIPVVLGPRAVYEDFVPPKSFIHVDDFKSPKELADYLLYLDTNPTAYS-----	301
Query:	312	PLNTLDGKAYFYQNLNSFKKILDFFKTILENDTIYHDNPFIIFYRDLNEPLISIDDLRVNYD	371
Sbjct:	302	-----EYFEWRYDLRVRLFSWDALR--YD	323
Query:	372	DLRVNYDDLRLRVNYDDLRLRVNYDDLRLRVNYD	399
Sbjct:	324	EGFCRVCRLLQNAPDRYKTYPNIAKWFQ	351

FIGURE 11

Protein sequence from strain 19C2 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	22	PPLNIALANWWPLDKRESKGFRKKFILHFILSQHYTIALHRNPDKPADIVFG-NPLGSAR	80
Sbjct:	12	VPLLLAIYTWWSL--IEYKEW-KKSPIYFIGSQAPQPPLR---ILLWTWPFGNPLALSD	65
Query:	81	KILSYQNAKRVFYTGEN---EVPNPNLF---DVAIGFDELDFRDRYLRMPLYYDRLHHKA	134
Sbjct:	66	CPLSYQNTARCRLLTANRSPLESADAVLFHHRDLSKGFPDLPSPRPPGQPWWASMESPS	125
Query:	135	ES-VNDTTAPYKIKSDSLYALKPSSHFKENPHLCALINNEIDPLKRGFASFVASNP-	192
Sbjct:	126	NSGLNDLRLDGYFNWTLSYRADSDAFHPYGYLEPRLSQVNVNAPLLSAKRKGAAWVVSNCNT	185
Query:	193	APIRNAFYEAALNSIEPVTVGGGSVRNLTGYNVKNKNEFLSQYKFNLCFENTQGYGYVTEKI	252
Sbjct:	186	RSKRERFYKQLNKHLQDVGGRVANPLPLKVGCCLVETLSQYKFYLAFENSQHYDYVTEKL	245
Query:	253	ID-AYFSHTIPIYWGGVPSVAKDFNP	277
Sbjct:	246	WKNALQAGTIPVVVLGP-RAVYEDFVP	270

FIGURE 12

	1	50
1111FutA.pep	(1) MFQPLLD A ^E IESAP I ^K KWPLN--LPPLKIAVANWWGDEE I ^K KK---FKKS V	
19C2A.pep	(1) MFQPLLD A ^E IESAP I ^K --	
915A.pepneose	(1) ----- A ^K MASK-SPPLKIAVANWWGDEE I ^K KK---FKKS V	
26695A.pep	(1) MFQPLLD A ^E IESAS T ^K MA S ^K KSPPPLKIAVANWWGDEE I ^K KE---FKKS V	
1182B.pep	(1) MFQPLLD A ^E IESAS T ^K IT S ^K KS-PPPLKIAVANWWGDEE I ^K EE---FKKN V	
1218B.pep	(1) MFQPLLD A ^E IESAS T ^K IT S ^K KS-PPPLKIAVANWWGDEE I ^K EE---FKKN V	
ORF19C2B.pep	(1) MFQPLLD A ^E IPSTR E ^D ETDYK--PPLNT A ^E ANWWPLDKRESKGFRKKF E	
Consensus	(1) MFQPLLD A ^E IESA IEK SK PPLKIAVANWWGDEI FKK I	
	51	100
1111FutA.pep	(46) LYFILSQHYT T ^I LHRNPDKP A ^D E ^I VFGNPLGSARKILSYQNAKRVFYTGEN	
19C2A.pep	(16) -----	
915A.pepneose	(29) LYFILSQHYT T ^I LHRNPDKP A ^D E ^I VFGNPLGSARKILSYQNAKRVFYTGEN	
26695A.pep	(48) LYFILSQRYA T ^I LHONPNEF D ^{EIVFSNPLGSARKILSYQNTKRVFYTGEN}	
1182B.pep	(47) LYFILSQHYT T ^I LHONPNEP D ^E I VFGSP E ^I GSARKILSYQNAKRVFYTGEN	
1218B.pep	(47) LYFILSQHYT T ^I LHONPNEP D ^E I VFGSP E ^I GSARKILSYQNAKRVFYTGEN	
ORF19C2B.pep	(48) LYFILSQHYT T ^I LHRNPDKP A ^D E ^I VFGNPLGSARKILSYQNAKRVFYTGEN	
Consensus	(51) LYFILSQHYT T ^I LH NP PADIVFGNPLGSARKILSYQNAKRVFYTGEN	
	101	150
1111FutA.pep	(96) EVPNFNLFDY A ^I IGEDELD F ^R DRYL M ^P LY Y ^A YL H ^M KAELVNDTTSPYKLQ	
19C2A.pep	(16) -----	
915A.pepneose	(79) EVPNFNLFDY A ^I IGEDELD F ^R DRYL M ^P LY Y ^A HL H ^M KAELVNDTTSPYKLQ	
26695A.pep	(98) ESPNFNLFDY A ^I IGEDELD F ^R DRYL M ^P LY Y ^A HL H ^M KAELVNDTTSPYKLK	
1182B.pep	(97) ESPNFNLFDY A ^I IGEDELD F ^R DRYL M ^P LY Y ^D RL H ^H KAESVNDTTSPYKLK	
1218B.pep	(97) ESPNFNLFDY A ^I IGEDELD F ^R DRYL M ^P LY Y ^D RL H ^H KAESVNDTTSPYKLK	
ORF19C2B.pep	(98) EVPNFNLFDY A ^I IGEDELD F ^R DRYL M ^P LY Y ^D RL H ^H KAESVNDTTSPYKLK	
Consensus	(101) E PN F NLF ^D Y A ^I IGEDELD F ^R DRYL M ^P LY Y ^D RL H ^H KAES VNDTTSPYKLK	
	151	200
1111FutA.pep	(146) PDSIYALKKP S ^H HEKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P RRN	
19C2A.pep	(16) -----	
915A.pepneose	(93) -----	
26695A.pep	(148) DNSIYALKKP S ^H HEKENHPNLCAVVNNEDS D L ^I KRGFASFVASNPNA P MRN	
1182B.pep	(147) PDSIYALKKP S ^H HEKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P KRN	
1218B.pep	(147) PDSIYALKKP S ^H HEKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P KRN	
ORF19C2B.pep	(148) SDSIYALKKP S ^H HEKENPHLCAVNNEIDPLIKRGFASFVASNPNA P IRN	
Consensus	(151) D S LYALKKP S ^H FKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P RN	
	201	250
1111FutA.pep	(196) AFYBALN A ^I EPVAGGGSV N ^T LGYN N ^K KNKSEELSOYKENICREN O GYGY	
19C2A.pep	(16) -----	
915A.pepneose	(93) -----	
26695A.pep	(198) AFYBALN A ^I EPVTGGGSV N ^T LGY K ^V GNKSEELSOYKENICREN O GYGY	
1182B.pep	(197) AFYBALNS I ^E PVIGGGSV N ^T LGYN N ^K KNKSEELSOYKENICREN O GYGY	
1218B.pep	(197) AFYBALNS I ^E PVIGGGSV N ^T LGYN N ^K KNKSEELSOYKENICREN O GYGY	
ORF19C2B.pep	(198) AFYBALNS I ^E PTGGGSV N ^T LGYN N ^K KNKSEELSOYKENICREN O GYGY	
Consensus	(201) AFYDALNSIEPV GGGSV K ^N T ^L GYN ^V KNKSEFLSQYKFNLCFENSQGYGY	

1111FutA 915A.cod (MWG) 19C2FutA.cod 26695A.cod 1182B 1218B.nuc ORF19C2B Consensus	1	50
	(1)	ATGTTCCAACCCCTATTAGATGCCTTATAGAAAGCGCT-CCATTGAAAA
	(1)	ATGTTCCAACCCCTATTAGATGCCTTATAGAAAGCGCTTCATTGAAAA
	(1)	ATGTTCCAACCCTTACTAGACGCCCTTATAGAAAGCGCTTCATTGAAAA
	(1)	ATGTTCCAACCCCTATTAGACGCCCTTATAGAAAGCGCTTCATTGAAAA
	(1)	ATGTTCCAACCCCTATTAGACGTTATATAGAAAGCGCTTCATTGAAAA
	(1)	ATGTTCCAACCCCTATTAGACGTTATATAGAAAGCGCTTCATTGAAAA
	(1)	ATGTTCCAACCCCTATTAGACGTTATATAGACAGCACCCGTTAGATGA
	(1)	ATGTTCCAACCCCTATTAGACGCCCTTATAGAAAGCGCTTCATTGAAAA
1111FutA 915A.cod (MWG) 19C2FutA.cod 26695A.cod 1182B 1218B.nuc ORF19C2B Consensus	51	100
	(50)	AATGGCCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT
	(51)	AATGGCCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT
	(46)	-----
	(51)	AATGGCCTCTAAATCTCCCCCCCCCCCCCTAAAATCGCTGTGGCGAATT
	(51)	AATTACCTCTAAATCTCCCCCCCCCCC-----TAAAAATCGCTGTGGCGAATT
	(51)	AATTACCTCTAAATCTCCCCCCCCCCC-----TAAAAATCGCTGTGGCGAATT
	(51)	AACCGATTATAA-----GCCCCCAT---TAAATATAGCCCTAGCGAATT
	(51)	AAT GCCTCTAAATCTCCCCCCCC TAAAAATCGCTGTGGCGAATT
1111FutA 915A.cod (MWG) 19C2FutA.cod 26695A.cod 1182B 1218B.nuc ORF19C2B Consensus	101	150
	(95)	GGTGG-----GGAGATGA-AGAAATTAAAAATTAAAAAGAGCGTTCTT
	(95)	GGTGG-----GGAGATGA-AGAAATTAAAAATTAAAAAGAGCGTTCTT
	(46)	-----
	(101)	GGTGG-----GGAGATGA-AGAAATTAAAAGAATTAAAAAGAGCGTTCTT
	(98)	GGTGG-----GGAGATGA-AGAGGTTGAAGAATTAAAAAGAACATTCTT
	(98)	GGTGG-----GGAGATGA-AGAGGTTGAAGAATTAAAAAGAACATTCTT
	(92)	GGTGGCCTTGGATAAAAGAGAAAGCAAGGGTTAGAAAAAAATTATTC
	(101)	GGTGG GGAGATGA AGAAATTAAAAGAATTAAAAAGA C TTCTT
1111FutA 915A.cod (MWG) 19C2FutA.cod 26695A.cod 1182B 1218B.nuc ORF19C2B Consensus	151	200
	(139)	T---ATTTTATCCTAACGCCAGCATTACACAATCAGTTACACGGAAACCC
	(139)	T---ATTTTATCCTAACGCCAGCATTACACAATCAGTTACACGGAAACCC
	(46)	-----
	(145)	T---ATTTTATCCTAACGCCAACGCTACGCCATTACACAATCAGTTACACGGAAACCC
	(142)	T---ATTTTATTCTCAGTCAGCATTACACAATCAGCCCTCCACCAAACCC
	(142)	T---ATTTTATTCTCAGTCAGCATTACACAATCAGCCCTCCACCAAACCC
	(142)	TTACATTTCAATTAGTCAGCATTACACAATCGCTCTCCACCGAAACCC
	(151)	T ATTTTAT CTAAG CAGCATTACACAATCAC CTCCACC AAACCC
1111FutA 915A.cod (MWG) 19C2FutA.cod 26695A.cod 1182B 1218B.nuc ORF19C2B Consensus	201	250
	(186)	TGATAAACCTGGGACATCGTCTTGGTAACCCCTTGGATCAGCCAGAA
	(186)	TGATAAACCTGGGACATCGTCTTGGTAACCCCTTGGATCAGCCAGAA
	(46)	-----
	(192)	CAATGAATTTCAGATCTAGTTTAGCAATCCTCTTGAGCGGCTAGAA
	(189)	CAAGGAACCTCCGATCTCGTCTTGGCAGTCCTATTGGATCAGCCAGAA
	(189)	CAAGGAACCTCCGATCTCGTCTTGGCAGTCCTATTGGATCAGCCAGAA
	(192)	TGATAAACCTGGGACATCGTTTGGTAACCCCTTGGATCAGCCAGAA
	(201)	AT AACCT C GA TCGTCTTGG AA CC CTTGGATCAGCCAGAA

FIG. 13 (1/6)

	251	300
1111FutA	(236) AAATCTTATCCTATCAAAACGCAAAAGGGTGTTCACCCGGTGAAAAT	
915A.cod (MWG)	(236) AAATCTTATCCTATCAAAACGCAAAAGGGTGTTCACCCGGTGAAAAT	
19C2FutA.cod	(46) -----	
26695A.cod	(242) AGATTTATCTTATCAAAACACTAAACGAGTGTTCACCCGGTGAAAAC	
1182B	(239) AAATCTTATCCTATCAAAACGCAAAAGAGTGTTCACCCGGTGAAAAC	
1218B.nuc	(239) AAATCTTATCCTATCAAAACGCAAAAGAGTGTTCACCCGGTGAAAAC	
ORF19C2B	(242) AAATCCTATCCTATCAAAACGCTAAAGGGTGTTCACCCGGTGAAAAC	
Consensus	(251) AAATCTTATCCTATCAAAACGCAAAAG GTGTTCACCCGGTGAAAAC	
	301	350
1111FutA	(286) GAAGTCCCTAACCTCACACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
915A.cod (MWG)	(286) GAAGTCCCTAACCTCACACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
19C2FutA.cod	(46) -----	
26695A.cod	(292) GAATCACCTAATTCACACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
1182B	(289) GAATCGCCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
1218B.nuc	(289) GAATCGCCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
ORF19C2B	(292) GAAGTCCCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
Consensus	(301) GAA CCTAACCTCTTGATTACGCCATAGGCTTT GATGAAT	
	351	400
1111FutA	(335) TGGACTTTAGAGATCGTTATTCAGAATGCCTTGATTATGCCATTG	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(341) TGGATTTAATGATCGTTATTCAGAATGCCTTGATTATGCCATTG	
1182B	(338) TGGATTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA	
1218B.nuc	(338) TGGATTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA	
ORF19C2B	(341) TGGACTTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA	
Consensus	(351) TGGA TTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA T	
	401	450
1111FutA	(385) CATTATAAGCCGAGCTTGTAAATGACACCCTCGCCTTATAAACTCCA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(391) CACTATAAGCCGAGCTTGTAAATGACACCCTCGCCTTACAACCTCAA	
1182B	(388) CACCATAAGCCGAGAGCGTGAATGACACCCTCGCCTTACAACCTCAA	
1218B.nuc	(388) CACCATAAGCCGAGAGCGTGAATGACACCCTCGCCTTACAACCTCAA	
ORF19C2B	(391) CACCATAAGCCGAGAGCGTGAATGACACCCTCGCAGCTTACAAGATCAA	
Consensus	(401) CAC ATAAAGCCGAG GT AATGACACCCT CGCCTTACAACCTCAA	
	451	500
1111FutA	(435) ACCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTAAAGAAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(441) AGACAACAGCCTTATGCTTTAAAAAAACCCCTCTCATCATTAAAGAAA	
1182B	(438) ACCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTAAAGAAA	
1218B.nuc	(438) ACCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTAAAGAAA	
ORF19C2B	(441) ATCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTAAAGAAA	
Consensus	(451) A CTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTAAAGAAA	

FIG. 13 (2/6)

		501	550
1111FutA	(485)	ACCACCCCAATTGTGCGCAGTAGTGAATAATGAGAGTGATCCTTGAAA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(491)	ACCACCCCTAATTGTGCGCAGTAGTGAATGAGAGCGATCTTTAAAA	
1182B	(488)	ACCACCCCAATTATGCGCAGTAGTGAACAATGAGAGCGATCCTTGAAA	
1218B.nuc	(488)	ACCACCCCAATTATGCGCAGTAGTGAACAATGAGAGCGATCCTTGAAA	
ORF19C2B	(491)	ACCACCCACATTATGCGCGCTAACATAATGAGATCGATCCTTGAAA	
Consensus	(501)	ACCACCC AATTT TGCGCAGTAGTGAA AATGAGAGCGATCCTTGAAA	
		551	600
1111FutA	(535)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTATGAGGAA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(541)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTATGAGGAA	
1182B	(538)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTAAAGGAA	
1218B.nuc	(538)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTAAAGGAA	
ORF19C2B	(541)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCCCTATAAGGAA	
Consensus	(551)	AGAGGGTTTGCAGCTTGTAGCGAG TTTGT GC AGCAACCTAACGCTCCTA AAGGAA	
		601	650
1111FutA	(585)	CGCTTTTATGAGGCTTAAACGCTATTGAGCCAGTTACTGGGGGAGGGA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(591)	CGCTTTTATGACGCTCTAAATTCTATAGAGCCAGTTACTGGGGGAGGAA	
1182B	(588)	TGCTTTCTATGACGCTTAAATTCTATAGAGCCAGTTACTGGGGGAGGGA	
1218B.nuc	(588)	TGCTTTCTATGACGCTTAAATTCTATAGAGCCAGTTACTGGGGGAGGGA	
ORF19C2B	(591)	CGCTTTCTATGAGGCTTAAATTCTATTGAGCCAGTTACTGGGGGAGGGA	
Consensus	(601)	GCTTT TATGA GCTTAAATTCTAT GAGCCAGTTA TGGGGGAGGGA	
		651	700
1111FutA	(635)	GCGTGAAAAACACTTTAGGCTATAATGTCAAAAACAAGAGCGAGTTTTA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(641)	GTGTGAGAAAACACTTTAGGCTATAAGGTTGGAAACAAAAGCGAGTTTTA	
1182B	(638)	GCGTGAAAAACACTTTAGGCTATAACATTAACAGAGCGAGTTTTA	
1218B.nuc	(638)	GCGTGAAAAACACTTTAGGCTATAACATTAACAGAGCGAGTTTTA	
ORF19C2B	(641)	GCGTGAGAAAACACTTTAGGCTATAACGTCAAAAACAAAAGCAATTTCG	
Consensus	(651)	GCGTGAA AACACTTTAGGCTATAA T AAAAACAA AGCGAGTTTTA	
		701	750
1111FutA	(685)	AGCCAATACAAATTCAATCTGTGTTTGAAAACACTCAAGGCTATGGCTA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(691)	AGCCAATACAAGTTCAATCTGTGTTTGAAAACACTCGCAAGGTTATGGCTA	
1182B	(688)	AGCCAATACAATTCAATCTGTGTTTGAAAACACTCAGAGGCTATGGCTA	
1218B.nuc	(688)	AGCCAATACAATTCAATCTGTGTTTGAAAACACTCAGAGGCTATGGCTA	
ORF19C2B	(691)	AGCCAATACAAGTTCAATCTGTGTTTGAAAACACTCAAGGCTATGGCTA	
Consensus	(701)	AGCCAATACAA TTCAATCTGTGTTTGAAAAC C CAAGGCTATGGCTA	

FIG. 13 (3/6)

		751		800
1111FutA	(735)	TGTAACTGAAAAGATCATTGACGCTTATTCAGCCATACCATTCCATT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(741)	TGTAACCGAAAAAAATCCTTGATGCGTATTTAGCCATACCATTCCATT		
1182B	(738)	TGTAACTGAAAAGATCATTGACGCTTACTTAGCCATACCATTCCATT		
1218B.nuc	(738)	TGTAACTGAAAAGATCATTGACGCTTACTTAGCCATACCATTCCATT		
ORF19C2B	(741)	TGTTACTGAAAAGATCATTGACGCTTACTCAGCCACACCATTCCATT		
Consensus	(751)	TGTAACTGAAAAGATCATTGACGCTTAAAGCCATACCATTCCATT		
		801		850
1111FutA	(785)	ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTAACCTAAGAGTTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(791)	ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTAACCTAAAAGTTT		
1182B	(788)	ATTGGGGG--AGTCC-TAGCGTGGCACAAAGATTTAACCTAAGAGTTT		
1218B.nuc	(788)	ATTGGGGG--AGTCC-TAGCGTGGCACAAAGATTTAACCTAAGAGTTT		
ORF19C2B	(791)	ATTGGGGGGAGTCCCTAGCGTGGCGAAAGATTTAACCCC-----		
Consensus	(801)	ATTGGGGG AGTCC AGCGTGGC AAGATTTAACCTAA AGTTTT		
		851		900
1111FutA	(832)	GTGAATGTCCATGATTCAACAACATTGATGAAGCGATTGACTATATCAG		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(838)	GTGAATGTGCATGATTCAACAACATTGATGAAGCGATTGATTATATCAA		
1182B	(835)	GTGAATGTTGTGATTAAAGATTTCATGAAGCGATTGATCATGTGCG		
1218B.nuc	(835)	GTGAATGTTGTGATTAAAGATTTCATGAAGCGATTGATCATGTGCG		
ORF19C2B	(832)	-----		
Consensus	(851)	GTGAATGT TGATT AA A TTTGATGAAGCGATTGA AT T		
		901		950
1111FutA	(882)	ATAC TTGCACACGCACCCAAACGCTTATTTAGACATGCACTATGAAAACC		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(888)	ATACCTGGACACGCACCCAAACGCTTATTTAGACATGCTCTATGAAAACC		
1182B	(885)	ATAC TTGCACACGCACCCAAACGCTTATTTAGACATGCTTATGAAAACC		
1218B.nuc	(885)	ATAC TTGCACACGCACCCAAACGCTTATTTAGACATGCTTATGAAAACC		
ORF19C2B	(832)	-----		
Consensus	(901)	ATAC TGCACACGCACCCAAACGCTTATTTAGACATGC TATGAAAACC		
		951		1000
1111FutA	(932)	CTTTAAACACTATTGATGGAAAGCTTACTTTACCAAATTTGAGTTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(938)	CTTTAAACACCCCTGATGGAAAGCTTACTTTACCAAAGATTGAGTTT		
1182B	(935)	CTTTAAACACCCCTGATGGAAAGCTTACTTTACCAAATTTGAGTTT		
1218B.nuc	(935)	CTTTAAACACCCCTGATGGAAAGCTTACTTTACCAAATTTGAGTTT		
ORF19C2B	(832)	-----		
Consensus	(951)	CTTTAAACAC TTGATGGAAAGCTTACTTTACCAA ATTTGAGTTT		

FIG. 13 (4/6)

		1001	
1111FutA	(982)	AAAAAAATCCTAGATTTTTAAAACGATTTAGAAAACGACACCGATCTA	1050
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(988)	AAAAAAATCCTAGATTTTTAAAACGATTTAGAAAACGATACGGATTTA	
1182B	(985)	AAAAAAATCCTAGATTTTTAAAACGATTTAGAAAACGACACCGATTTA	
1218B.nuc	(985)	AAAAAAATCCTAGATTTTTAAAACGATCTAGAAAACGACACCGATTTA	
ORF19C2B	(832)	-----	
Consensus	(1001)	AAAAAAATCCTAGATTTTTAAAACGAT TTAGAAAACGA ACGAT TA	
		1051	
1111FutA	(1032)	TCACGATAACCC-----TTTCATTTCTATCGTATTGAATGAGCCTT	1100
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1038)	TCACAAATTCTCAACATCTTCATGTGGGAGTACGATCTGCATAAGCCGT	
1182B	(1035)	TCACGATAACCC-----TTTTATTTTTATCGTATTGAATGAGCCTT	
1218B.nuc	(1035)	TCACGATAACCC-----TTTTATTTTTATCGTATTGAATGAGCCTT	
ORF19C2B	(832)	-----	
Consensus	(1051)	TCAC A C C TTT AT T A GAT TG AT AGCC T	
		1101	
1111FutA	(1076)	CAGTATCTATTGATGGT---TTGAGGGTTAACATTATGATGATTGAGGGTT	1150
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1088)	TAGTATCCATTGATGAT---TTGAGGGTTAACATTATGATGATTGAGGGTT	
1182B	(1079)	TAATATCTATTGATGATGATTGAGGGTTAACATTATGATGATTGAGGGTT	
1218B.nuc	(1079)	TAATATCTATTGATGAT---TTGAGGGTTAACATTATGATGATTGAGGGTT	
ORF19C2B	(832)	-----	
Consensus	(1101)	A TATC ATTGATG T TTGAGGGTTAACATTATGATGATTGAGGGTT	
		1151	
1111FutA	(1123)	AATTATGATGATTGAGGGTTAACATTATGATGATTGAGGGTTAACATTATGA	1200
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1135)	AATTATGACCGGCTTTACAAAACGCCCTCGCCTTATTAGAACTCTCTCA	
1182B	(1129)	AATTATGATGATTGAGGGTTAACATTATGATGATGATTGAGGGTTAACATTATGA	
1218B.nuc	(1126)	AATTATGATGATTGAGGGTTAACATTATGATGATGATTGAGGGTTAACATTATGA	
ORF19C2B	(832)	-----	
Consensus	(1151)	AATTATGA T AA T TTT G T T A	
		1201	
1111FutA	(1173)	GCGCCTTTACAAAACGCCCTCGCCTTATTAGAACTCTCTCAAAACACCA	1250
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1185)	AAACACCACTTTAAAATCTATCGCAAAGCTTATCAAAATCCTGCCTT	
1182B	(1179)	TGATTGAGGGTTAACATTATGATGATTGAGGGTTAACATTATGATGATTGA	
1218B.nuc	(1176)	TGATTGAGGGTTAACATTATGATGATTGAGGGTTAACATTATGATGATTGA	
ORF19C2B	(832)	-----	
Consensus	(1201)	AA	

FIG. 13 (5/6)

		1251		
1111FutA	(1223)	CTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCTTGCGT		1300
915A.cod(MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1235)	TGTTGCGCGCGGTGAGAAAGTTGGTTAAAAAATTGGGTTTGTA-----		
1182B	(1229)	GGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAAT		
1218B.nuc	(1226)	GGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAAT		
ORF19C2B	(832)	-----		
Consensus	(1251)	T	T A A	
		1301		1350
1111FutA	(1273)	GCCATAAGGAGATGGGTTAAAAAGTAA-----		
915A.cod(MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1279)	TATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGAGCG		
1218B.nuc	(1276)	TGTGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGAGCG		
ORF19C2B	(832)	-----		
Consensus	(1301)			
		1351		1400
1111FutA	(1300)	-----		
915A.cod(MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1329)	GCTCTTACAAAACGCCCTCGCCTTATTAGAACCTCTCTCAAAACACCACTT		
1218B.nuc	(1326)	GCTCTTACAAAACGCCCTCGCCTTATTAGAACCTCTCTCAAAACACCACTT		
ORF19C2B	(832)	-----		
Consensus	(1351)			
		1401		1450
1111FutA	(1300)	-----		
915A.cod(MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1379)	TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTGCGTGC		
1218B.nuc	(1376)	TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTGCGTGC		
ORF19C2B	(832)	-----		
Consensus	(1401)			
		1451		1483
1111FutA	(1300)	-----		
915A.cod(MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1429)	GCGAGAAAGTTGATTAAAAATTGGGTTTGTA		
1218B.nuc	(1426)	GCGAGAAAGTTGATTAAAAATTGGGTTTGTA		
ORF19C2B	(832)	-----		
Consensus	(1451)			

FIG. 13 (6/6)

Oligo Structures

Lacto-N-neo-Tetraose (LNnT)

Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc

Lacto-N-Fucopentaose III (LNFP III)

Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc

3

|

1 α Fucose

FIG. 14

Linkage Analysis by GC/MS

The samples were methylated, hydrolyzed, reduced with sodium borodeuteride, acetylated and analyzed by GC/MS along with samples of LNNT and LNF3.

- A Glc vs. Glc-NAc value close to 1 favors fucosylation of Glc-NAc.
- A Glc vs. Glc-NAc value close to 0 favors fucosylation of Glc

<i>H. Pylori</i> Strain	Glc vs. Glc-NAc
915A2	0.982
19C2A5	0.040
1111A2	0.975
19C2B1	0.991
1182B3	0.983

FIG. 15

1 Liter LNFIII Synthesis

Batch Number	Resin Type	Total Yield	Actual Percent Recovery
1-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.567 g	61%
2-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.760 g	68%
3-02	Dowex1/Dowex 50 (2ml resin/1ml synthesis)	1.221 g	47%

FIG. 16

FIG. 17

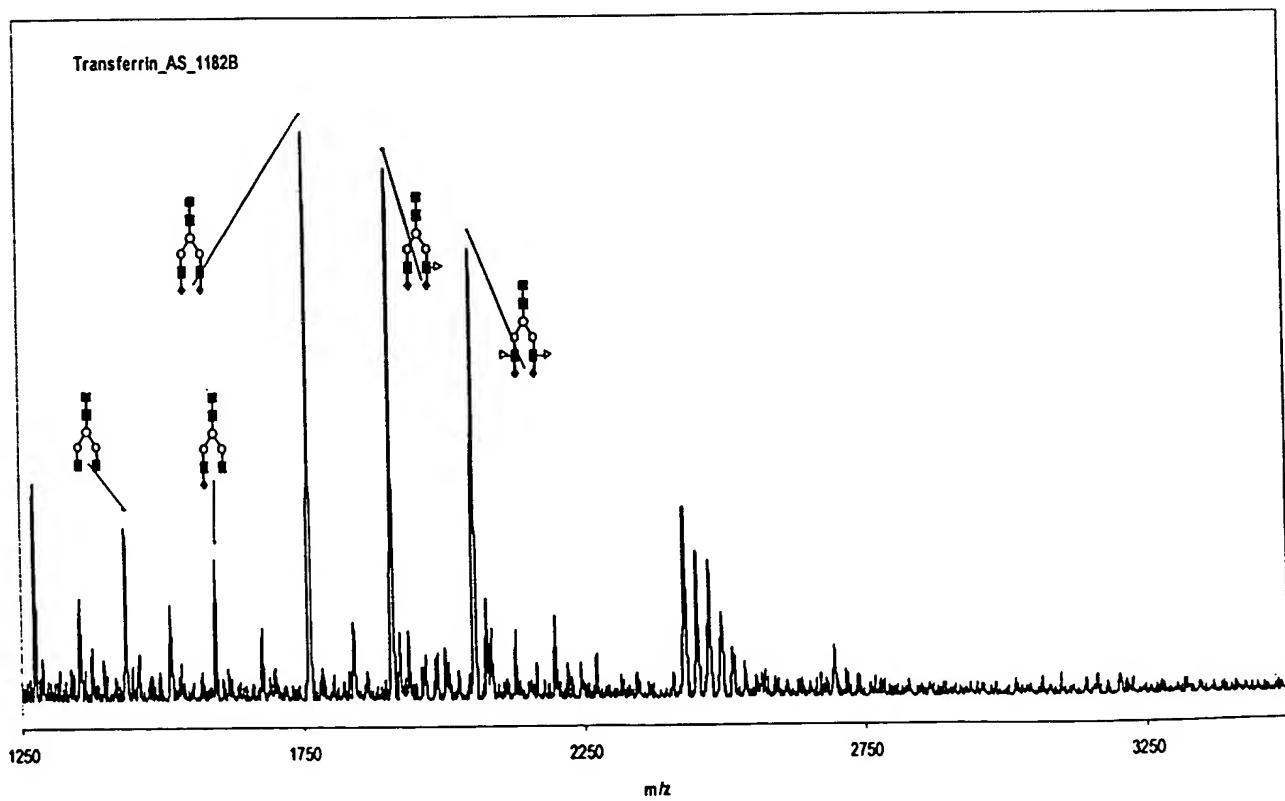
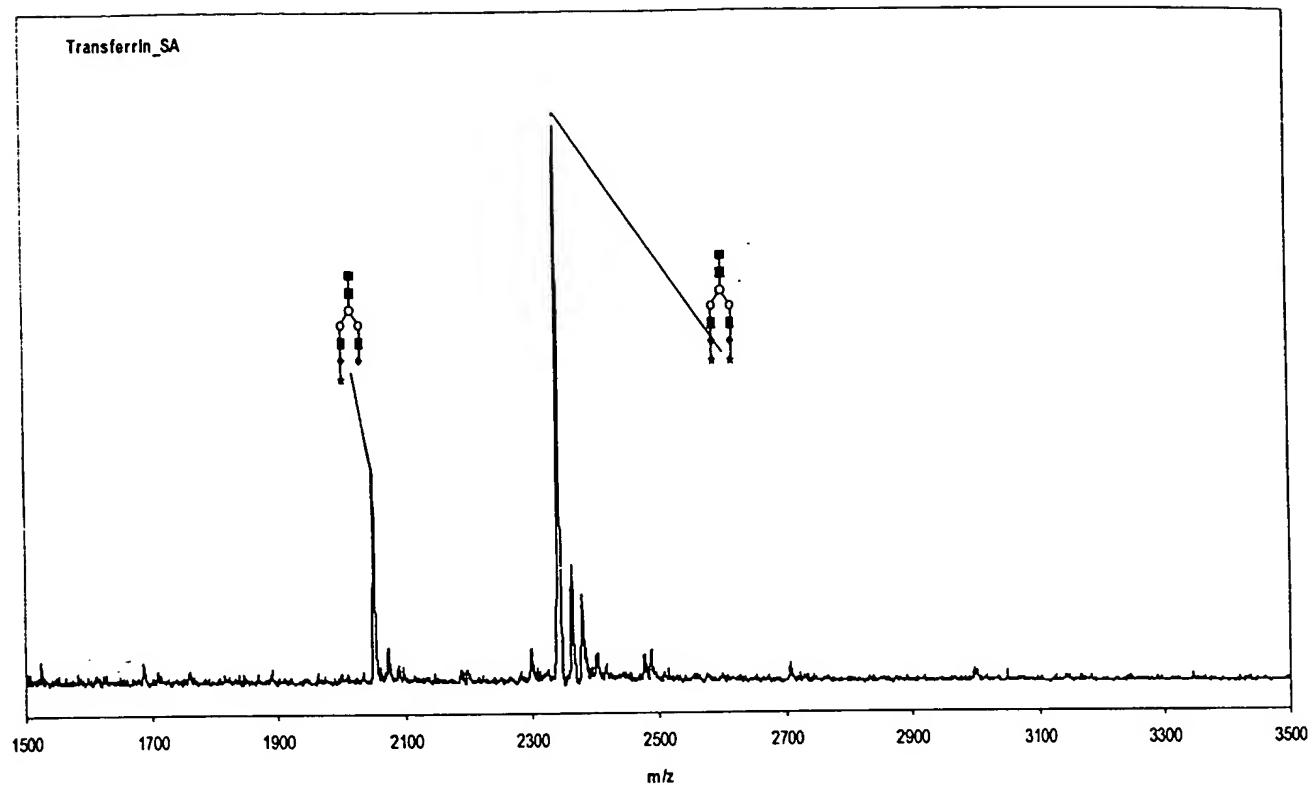


FIGURE 18

Strain 1111FutB fucosyltransferase nucleotide coding sequence (SEQ ID NO:15)

ggatccCGAGCGACCAATCATTACAGGGATTATTGCATTAGATGCGGCTTCAGTAACACGCTGATCGT
GGAAAATAACGCCAACCGCTTGGTTACCGGGCATATGATGTTTACATTCTAAAGGGCAAATGCTCC
TCGCTTGCAACGCTCGTTGAATATCAGTAAAGATCGCACTTAGTCGTGGCGATGGGGCAATGATTG
AGCATGTTAACACATGCCCATATTAAAATCGCTTCAACGCTAAAGAGGTTTAAAACAGCACGCCACGCA
TTGCATCAATGAGCCTAATCTAGCCCTAATCAAGCCTTGATTACAAAATTTTTGTAACATTCCCT
TTAAAAGGATAGCCatgttccaacccctattagacgcttagttagaaagcgcttcattgaaaaaatggcc
tctaaatctccccccccctaaaatcgctgtggcaattgggtggggagatgaagaaattaaagaattaa
aaagagcgttctttatttatcttagccaacgcacacaatgcctccaccaaaaccccaatgaatttt
cagatctagtcttagcaatcccttgatcagctagaaaaatcttatcgatcaaaacgcataaagagtg
tttacaccggtaaaatgaagtccctaacttcaacctctttagtacgccttaggctttagtgaatttgg
tttagagatcgttattttaggatgccttattatgataggctacaccataaagccgagagcgtgaatg
acaccacttcgcctacaaactcaaagacaacgccttatactttaaaaaacccctccatcaattaaa
aaaaaccaccctaatttagcgcagtcgtgaatgatgagagcgtcccttggaaaagaggggttgtgagctt
gtagcgagcaacgcataacgcctcatgagaaacgcctttatgacgctttaattctattgagccagttac
tgggggagggagcgtaaaaacactttaggctataacgtcaaaaacaagagcgttttaagccaaataca
agttcaacctgtgtttgaaaactcacaaggctatggctatgttaaccgagaagatcctgacgcttacttt
agcccacaccattctattttagggggagtcctagcgtggcgaaagatttacccctaaagagttgtgaa
tgtccatgattcaacaactttagtgaagcgatagattatataaataacttgcacacgcacccaaacgcct
atttagacatgctctatgaaaaaccctttaacgcctttagggaaagcttactttaccaggatttgagt
ttaaaaaaaaatcctagctttttaaaacgattttagaaaacgatacgcattatcacaatcccaacatc
tttcatgtggagtgcgtctcgatgagccgttagcgtctattgatgatttgagggttaattatgatgattt
gagggttaattatgatgattttagggtaattatgatgattttagggtaattatgatgattttagggta
attatgatgattttagggtaattatgatgctttgcacaaacgccttacccatttggaaattatcccaa
acacctttttaaatctatcgcaaaaggctatcacaaggctatcacaatccctacccttattgcgcgcac
aaGGAGATGGGTTAAAAGTAAGGTGCTTTAAAGACTGGGTGAGAAATTGAAGCGCTATTAAAAATGCG
CTAACCGCTCTTTTGAGCGTGGGGTTTGAGCATGTCCTCTAAAGCATGGGCCTTAAAAAAATGTTG
GATTTAAAGACACGATGCCCAAGGATTCTCTTAGAAAGGTTAAAAGGCCTTGGGCAAAATCTC
GCCAAATACGATAATGACTTTGAAGCGCTGTTGCTAATTGCCAGGTCGgaattc

Strain 1111FutB fucosyltransferase amino acid sequence (SEQ ID NO:16)

MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFISQRYTIALHQNPNEFSDLVF
SNPLGSARKILSYQNAKRVFTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHKAESVNDTSP
YKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESPLKRGVVSVVASNANAPMRNAFYDALNSIEPVGGGS
VKNTLGYNVKNKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGPSVAKDFNPKEFVNVDHF
NNFDEAIDYIKYLHTHPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWE
CDLDEPLASIDDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYERLLQNASPILLELSQNTSF
KIYRKAYQKPIKNPYPYCAP

FIGURE 19

Strain 802FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:17)

ggatccCGGCGTGAATTACTACCTTCTGGCTTGACAGCTATGCCGAGGCATCCCTGCCTATCCCTA
CTTCTTATACTTTGGTAGCGATACTTTGCTCTCGTATTGGCTATTCAAACGCCATTGAGT
TTGCCCTAAATTGGTTAAAGGATAGCCTGTTCCAGCCCTACTAGACGCCCTTATAGAAAGTGCCTCAAT
TAAAAAAATGCCCTGTAGTTACCCCCCTAAAATGCCGTGGGAATTGGTGGGGAGGCCTGAAGAAT
TTAAAAAGAGCGCTATGTATTCTAAGCCAACGCTACACAATCACCCACCAAAACCCCAACGAA
CCCTCCGATCTGTCTTGGCAGTCCTATTGGAGCAGCAGAAAAATCCTATCCTACCAAAACACTAAAAG
AGTGTGTTACGCCGGTAAAAATGAAGTCCCTAATTCAACCTTTGATTACGCCATAGGCTTGATGAAT
TGGATTTAGAGATCGTTATTGAGAATGCCCTTATATTGATAGACTACACCATAAGCCGAGAGCGTG
AATGACACCACCGCGCCTACAAGATTAACCTGACAGCCTTATACCTTAAAAAACCTCCCATTCAATT
TAAAGAAAAACACCCCCATTATGCGCAGTAGTGAATGATGAGAGCGATCCTTGAAGAGGGTTGCGA
GTTTGTGCAAGCAACCTAACGCCCTAAAAGGAACGCCCTATGACGCTTAAATTCTATTGAGCCA
GTTACTGGGGGAGGGAGCGTGAACCAACTTCTAGGCTATAAGTGGAAACAAAACGAGTTTTAAGCCA
ATACAAATTCAATCTGTGTTTGAACACTCTCAAGGCTATGGCTATGTAACCGAAAAATCATTGACGCTT
ACTTCTAGCCATACCATTCTATTGAGGGAGTCCTAGCGTGGCAAAGATTAAACCTAAGAGTTT
GTGAATGTGATGATTAAAAACTTGTAGAAGCGATTGATTACGTGAGATACTTGACACGCACCCAAA
CGCTTATTAGACATGCTCTATGAAACCCCTTAAACACCCCTGATGGGAAAGCTTACTTTACCAAGATT
TGAGTTTAAAAAAATCCTAGATTGAGGTTAAACGATTTAGAAAACGATACGATCTATCACAATAACCC
TTTGTGTTCTATCGTGAATTGAGCGTTAGTATCTATTGATGATTGAGAGCGATTATAATAATT
GAGAGCCGATTATAATAATTGAGAGCCGATTATAATAATTGAGAGCCGATTATAATAATTGAGAGCCG
ATTACGATGCCGTTACAAACCGTTGCCCTTGGAACTCTCTAAACACCCACTTTAAATCTAT
CACAAAGCTTATCACAAATCCTTACCTTGTGCGTGCATAAGGAGATGGGTTAAAAAATGGGTTTGta
aATTGGGGTAATCAAACCCCTGCGTATCATCGCAGACGCCACTTTCTAAACCAAGCGATATTAGCC
CCTAAACAAATTAGTAGGGTCTTAAACTCTTGTGAGAGACATTAAATCTCTTCA
GATGTGGTGTAAATTCCGATCCACCACTTCAAAACTCCAAGGGTGCATGCTCGCTTGCCTGCGCATTCCA
AGCCGCTCACGCTACCCCCCAGCATTAGCCGCTTGCCTACCCATAAGAAATCTAGCCTGAAAAAC
AATTCAATCGCTTATTGCTTGAGGGCATGTTGCCCCCTCAGCCACGCATTGACCCATTAGAAAGGAG
GGTTTGCgaaattc

Strain 802FutA fucosyltransferase amino acid sequence (SEQ ID NO:18)

MFQPLLDLAFIESASIKMPLSYPLKIAVANWWGAEFFKSAMYFILSQRYTITLHQNPNEPSDLVFGSP
IGAARKILSYQNTKRVFYAGENEVPNFNLFDYAI GFDELDLDRYLRMPLYYDRLHHKAESVNDDTAPYKI
KPDSLYTLKKPSHHFKEKPHLCAVNDESPLKRGFASFVASNPNA PKRNAFYDALNSIEPV TGGGSVKN
TLGYKVGKNEFLSQYKFNLCFENSQGYGYTEKIIDAYFSHTIPIYWGPSVAKDFNPKSFVNVDHFKNF
DEAIDYVRLHTPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNE
PLVSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYDRLLQNRSPLLELSQNTTFKIYHKAYHKSLP
LLRAIRRWVKLGL

FIGURE 20

Strain 948FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:19)

Strain 948FutA fucosyltransferase amino acid sequence (SEQ ID NO:20)

MQPPLDAFIDSTHLDDETTKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILHSNPNEPSDLVF
GNPLEQARKILSYQNTKRVFTYGENEVPNFLFDYAIGFDELFNDRFLRMPLYAYLHYKAMLVNDTSP
YKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGFASFASNPNAPIRNAYFDALNAIEPVASGGSVK
NTLGYKVKNKNEFLSQYKFNLCFENSQGYGVTEKILDAYFSHTIPIYGSPSPVAKDFNPKSFVNVDFFNN
FDEAIDYIRYLHAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR
DLNEPLVSDDLRRDHDDLRVNYDDLRLRVNYDDLRLRVNYDDLRRDHDDLRDHERLLSK
ATPLLELSQNTSFKIYRKAYQKSLPLLRAI

FIGURE 21

Strain 955FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:21)

ggatcccGAGCAGCAATCATACAGGGATTATAAATTAGATGGCTTCAGTAACACGCTGATAGT
GGAAAATGGTGCCTTAAACGGCTGGTTACGGGCATATGATGTTTCACACTCTAAAGGCAGATGCTTC
TCGCCCTACAACGCTTGCTAAATATCAGTGAAACGAGCACTTAGTGTGGCGATGGAGCGAATGACTTG
AGCatgttCAAACATGCCATATAAAATCCTCAACGCTAAAGAGGTTTAAACAACAGCCACCGCA
TTGCATCAATGAGCCTGATTAGCCCTAACAGCCTTGAATTAAAAAATTTTTGTAAAATACTCCT
TTAAAGGATAAAAGATGTTCCAGCCCCTATTAGATGCTTCATAGAAAGCCTCAATTAAAAAAATTGC
CTCTAAATCTCCCCCCCCCTAAAAATCCTGTGGCGAATTGGTTAACGGCACTAAAGAATTAAAGCGAG
CGTTCTTATTCATCTAAACACGCTATAAAATCATTCTGCACAGCAACCCCTAATGAACCCCTCAGATC
TAGTCTTGGCAATCCTTGGAAACAAGCCAGAAAAATCTTATCTTATCAAAACACTAAACGAGTGTTCAC
ACCGGCAGAAATGAAGTGCCTAATTCAATCTCTTGATTACGCCATAGGCTTGTGAATTGGATTAA
CGATCGTATTTGAGAATGCCCTTGATTACGCCATTGCAATTAAAGCCATGCTTGTAAATGACACCA
CTTCGCCCTATAAAACTCAAAGCCTTTACTTTAAAAAAACCTTCCCTAAATTAAAGAAAACCACCCC
AATTATGTGCGCTAATCCATAACGAGAGCGATCCTGGAAAAGAGGTTGCCAGTTGCGAAGCAA
TCCTAACGCTCCCATCAGAAACGCTTCTATGACGCTTAAATGCTATTGAGCCAGTGGCTAGTGGAGGG
GTGTAAAAACACTCTAGGCTATAAGGTCAAAACAAAAACGAATTAAAGCCAAATACAAGTTCAACCTC
TGTTTGAAAACCTACAAGGCTATGGCTATGTAACGAAAAAATCCTTGATGCGTATTCAAGCCACACTA
TCCCTATTATGGGGAGTCCAGCGTGGCGAAAGATTAAACCCCTAAAGTTGTGAATGTCATGAT
TTCAACAACTTGTATGAAGCGATTGATTATCAGATATTACACGCCACCAAACGCTTATTAGACAT
GCTTATGAAAACCCCTTAAACACCATTGATGGAAAGCGGGTTTACCAAGATTGAGTTGAAAAGA
TCTTAGATTTTCAAAACATTCTGAAAACGATACGATTATCATTGCAATGATGCCATTATTCTGCT
CTTCATCGTATTGAATGAGCGTTAGTGTCTGTGATGATTGAGAAGAGATCATGATGATTGAGGGT
TAATTATGATGATTGAGAAGAGATCATGAACGCCCTTATCAAAGGCTACCCCTTTGGAGCTATCCC
AAAACACCTTTAAATCTATCGCAAAGCTTACAAAGTCTTACCCCTGTGCGTCATAAGGAAG
TGGGTTAAAAAATAAGCGTATTTAAGACTGATGAAGAAATTGAAGCGCTATTAAATGCGCTAACGC
TTCTTTTGAGCGTGGGGTTTGTGAGCATGTCCTAAAGCATGGGTGCTTAAAAAATGTTGTTTTA
AAGACACGATGCCCTCAAAGGATTCTCTTAAAGGTTAAAAGCGTTGGGCAAATCTGCCAAAT
ACCACAAATGACTTTGAAGCGTGTGCTAATTGCCAGGTCGgaattc

Strain 955FutA fucosyltransferase amino acid sequence (SEQ ID NO:22)

MFKHAHIKIAFNAKEVLKQHATHCINEPDALALIKPLIFKIEFKYVSFKG. RCSSPY. MPS. KALQLKKNCL
ISPLKIAVANWFNGTKEFKASVLYFILKQRYKIIILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYT
GENEVPNFNLFDYAI GFDELD FNDRYL RMLP YYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPN
LCALIHNESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNL
FENSQGYGYVTEKIP. CVFQPHYPYLLGESQRGERF. P. KFCECA. FQQL. SD. LYQIFTRAPKRLFRHA
L. KPLKHH. WESGFLPRFEF. KDLRFQKHS. KRYDLSLQ. CPLFCSSS. FE. AVSVC. FEKRS. FEG.
L. FEKRS. TPLIKGYPSTGAIPKHLF. NLSQSLSKVLTUVACHKEVG. KIRRII LRLMKKLKRYFKMR. RF
FFERGVFEHVL. SMGA. KMFCF. RHDAKGFFF RKV. KA FGQNLAKYHND. SAVV. LPGRN

FIGURE 22

Strain 1218FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:23)

ggatccTCTGGCTTGACAGCTATGCCGAGGCATCCCTGCCTATCCCTACTTTCTTATACTTTGG
TAGCGATACCTTCGCTCTCGTGTCTGGTTATTCAAACGCCATTGAGTTGCCTAAATTGGTTAA
AGGATAACCAGTTCACCCCTATTAGCCTTATATAGAAAAGCCTTCAATTGAAAAAATTACCTCTAA
ATCTCCCCCCCCCTAAAATCGCTGGCGAATTGGTGGGAGATGAAGAGGTTGAAGAATTAAAAAGA
ACATTCTTATTATTCTCAGTCAGCATTACACAATCACCCCTCCACCAAAACCCAAACGAACCCCTCGAT
CTCGTCTTGGCAGTCCTATTGGATCAGCCAGAAAAATCTTATCCTATCAAACGCCAAAGAGTGTGTTA
CACCGGTGAAAAGAATGCCATTCAACCTCTTGTATTACGCCATAGGTTGATGAATGGATTAG
AGATCGTTATTAAGAATGCCATTATATTGATAGACTACACCATAAGCCGAGAGCGTGAATGACACCA
CTTCGCCTTACAAACTCAAACCTGACAGCCTTATGCTTTAAAAACCCCTCCCATATTAAAGAAAAC
CACCCCAATTATGCGCAGTAGTGAACAATGAGAGCGATCCCTTGAAGAGGGTTGCGAGTTGTAGC
GAGCAACCTAACGCTCCTAAAAGGAATGCTTCTATGACGCTTAAATTCTATAGGCCAGTTATTGGGG
GAGGGAGCGTGAACACTTAGGCTATAACATTAAAACAAGAGCGAGTTTAAGCCAATACAAATT
AATCTGTGTTTGAACACTCACAAGGCTATGGCTATGTAAGTGAACCTACATTGACGCTTACTTTAGCA
TACCATCCATTATTATTGGGGGAGTCCTAGCGTGGCACAAGATTAAACCTAAGAGTTGTGAATGTT
GTGATTAAAGATTGATGAAGCGATTGATCATGTGCGATACTTGACACGCCAACGCTTATT
GACATGTTATGAAAACCTTAAACACCCTGATGGAAAGCTTACTTTCAAAATTGAGTTTAAAA
AAATCTAGATTAAACGATCTAGAAAACGACACGATTATCAGATAACCTTTATTGTT
CGTGATTGAATGAGCGTTAATATCTATTGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATT
TGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATT
TGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTT
AATTGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGAGCGCTTACAAAACGCTC
GCCTTATTAGAACCTCTCAAAACACCACTTTAAATCTATCGCAAAGCTTACAAAATCCTTACCTT
TGTTGCGTGGCGAGAAAGTGTATTGAGGGTTAATTGAGGGTTAATTATGATGATTGAGGGTT
TATCATCGCAGGCCACCTTCTAAAACAGCGATATTAGCCCCTAAACAAAATTAGTAGGGTCTTAA
ACTCTTAGCGGTTTGAGAGACATTCTTATAAgaattc

Strain 1218FutA fucosyltransferase amino acid sequence (SEQ ID NO:24)

MFQPLLDAYIESASIEKITSKSPPPLKIAVANWWGDEEVEFKKNILYFILSQHYTITLHQNPNEPSDLVF
GSPIGSARKILSYQNAKRVFYTGENSEPNFNLFDYAIGFDEWILEIVI.ECLYIMIDYTIKPRA.MTPLRL
TNSNLTAFML.KNPPILKKTTPIYAQ..TMRAIL.KEGLRVL.RATLTLKGMLSMTL.IL.SQLLGEGA
.KTL.AITLKTRASF.ANTNSICVLKTHKAMAM.LKKSLTTLAIPFLFIGGVLAWHKILTLRVL.MFVIL
KILMKRLIMCDTCRTQTLLI.TCFMCTL.TPLMGKLTQNLFSKKILDFFKTILENDTIYHDNPFIIFYRDL
NEPLISIDDLRVNYDDLDRVNYDDLDRVNYDDLDRVNYDDLDRVNYDDLDRVNYDDLDRVNCDD
DLRVNYDDLDRVNYERLLQNAPLLELSQNTTFKIYRKAYQKSLPLLRAARKLIKLLGL.NWG.SNPLRYHR
RRHLSKTS DISP.NKISRVFKLFSGLRDILIRIRYQAYRYRRPRGGAR